Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1. (currently amended) A method of identifying a compound that stabilizes an α-helical conformation of a discordant helix in a polypeptide, the method comprising:

(a) providing a test sample *in vitro* comprising a polypeptide that contains a discordant helix in the form of an α-helix;

(b) contacting the test sample with a test compound; and

(c) determining the rate of decrease in the amount of α-helix in the test sample,

wherein a lower rate of decrease in the presence of the test compound than in the absence of the test compound is an indication that the test compound stabilizes the α-helical conformation of the discordant helix in the polypeptide.

2. (currently amended) A method of identifying a compound that can stabilize the α-helical conformation of a discordant helix-containing polypeptide, the method comprising:

a) providing a test sample *in vitro* comprising a polypeptide that contains a discordant helix in the form of an α-helix;

b) contacting the test sample with a test compound; and

c) determining the amount of α-helix present in the test sample,

wherein a higher amount of α-helix remaining in the presence of the test compound than in the absence of the compound indicates that the test compound stabilizes the α-helical conformation of the discordant helix in the polypeptide.

3. (withdrawn) A compound identified by the method of claim 1.

4. (withdrawn) A compound identified by the method of claim 2.

5. (withdrawn) A method of identifying whether a protein is susceptible to forming amyloid, the method comprising analyzing the amino acid sequence of the protein to determine whether the protein contains a predicted discordant helix, wherein the presence of predicted discordant helix is an indication that the protein is susceptible to forming amyloid.

6. (withdrawn) The method of claim 5, wherein the discordant helix is at least six amino acids in length.

7. (withdrawn) A method of decreasing the rate of formation of β-strand structures between at least two discordant helix-containing polypeptides, the method comprising contacting the discordant helix-containing polypeptides with a compound that stabilizes an α-helical form of the discordant helix.

8. (withdrawn) A method of treating an individual having or at risk for an amyloidosis, the method comprising administering to the individual a therapeutically effective amount of a compound that stabilizes an α-helical form of a discordant helix-containing polypeptide that forms amyloid.

9. (withdrawn) The method of claim 8, wherein the amyloidosis is selected from the group consisting of prion diseases and Alzheimer's disease.

10. (new) The method of claim 1 or claim 2, wherein the polypeptide that contains a discordant helix is an Aβ peptide.

11. (new) The method of claim 1 or claim 2, wherein the polypeptide that contains a discordant helix is Aβ(1-40).

12. (new) The method of claim 1 or claim 2, wherein the polypeptide that contains a discordant helix comprises residues 14-23 of Aβ peptide.

13. (new) The method of claim 1 or claim 2, wherein the polypeptide that contains a discordant helix comprises residues 16-23 of Aβ peptide.

14. (new) The method of claim 1 or claim 2, wherein the polypeptide that contains a discordant helix is prion protein (PrP) or surfactant associated protein (SP-C).

15. (new) The method of claim 1 or claim 2, wherein the test compound is a peptide.

16. (new) The method of claim 1 or claim 2, wherein the test compound is a tripeptide.

17. (new) The method of claim 1 or claim 2, wherein the test compound is a dipolar tripeptide.

18. (new) The method of claim 1 or claim 2, wherein the test compound is a tetrapeptide.

19. (new) The method of claim 1 or claim 2, wherein the test compound comprises the amino acid sequence KAD.

20. (new) The method of claim 1 or claim 2, wherein the test compound comprises an amino acid sequence selected from the group consisting of KFD, DAK, DFK, RAD, RFD, DAR, DFR, KAE, KFE, EAK, EFK, RAE, RFE, EAR, or EFR.

21. (new) The method of claim 1 or claim 2, wherein the test compound comprises a tripeptide in which the middle residue is an uncharged residue.

22. (new) The method of claim 15, wherein the peptide has protected termini.

23. (new) The method of claim 1 or claim 2, wherein the test compound interacts with Lys16 and Glu22/Asp23 of an Aβ peptide.

24. (new) The method of claim 1 or claim 2, wherein the test compound is a peptidomimetic, small molecule, or antibody.

25. (new) The method of claim 1 or claim 2, wherein the test compound is a monoclonal antibody.

26. (new) The method of claim 1, wherein the rate of decrease in the amount of α-helix in the test sample is determined using electrospray (ES)-mass spectroscopy or matrix-assisted laser desorption/ionization (MALDI) mass spectroscopy.

27. (new) The method of claim 1, wherein the rate of decrease in the amount of α-helix in the test sample is determined using circular dichroism (CD), infrared spectroscopy, Fourier transform infrared spectroscopy (FTIR), or nuclear magnetic resonance (NMR).

28. (new) The method of claim 1, wherein the rate of decrease in the amount of α-helix in the test sample is determined using hydrogen to deuterium (H/D) exchange mass spectroscopy.

29. (new) The method of claim 2, wherein the amount of α-helix in the test sample is determined using electrospray (ES)-mass spectroscopy or matrix-assisted laser desorption/ionization (MALDI) mass spectroscopy.

30. (new) The method of claim 2, wherein the amount of α-helix in the test sample is determined using circular dichroism (CD), infrared spectroscopy, Fourier transform infrared spectroscopy (FTIR), or nuclear magnetic resonance (NMR).

31. (new) The method of claim 2, wherein the amount of α-helix in the test sample is determined using hydrogen to deuterium (H/D) exchange mass spectroscopy.

32. (new) The method of claim 1, further comprising determining the rate of fibril formation in the presence and absence of the test compound.

33. (new) The method of claim 2, further comprising determining the amount of fibril formation in the presence and absence of the test compound.